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Quest for SARS source gathers pace in bid to thwart resurgence

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At least three species of wild animals sold in markets in the Guangdong province of southern China have been shown to harbour the virus that causes severe acute respiratory syndrome (SARS). And a substantial number of similar leads are being developed, according to an international delegation of experts.

The delegation was in Guangdong, where the SARS outbreak began, this month to assess the progress being made in the hunt for the disease's animal 'reservoir'. Like flu, SARS is suspected to be seasonal. But the group found that as winter approaches, local scientists are a long way from identifying which species is the true reservoir for the disease — and so could spark a fresh SARS outbreak.

Several Chinese research institutes have been involved in the intense effort to test both domesticated and wild animals for the coronavirus that causes SARS. And the delegation, split half-and-half between Chinese researchers and those from elsewhere, representing the World Health Organization (WHO) and the United Nations Food and Agriculture Organization, was surprised by some of the results it was shown.

At a press conference on 20 August, the visiting scientists discussed the wide range of animals — from snakes through to mammals — that have been tested for the SARS coronavirus so far. Most of the results were negative, but a surprising number of species tested positive, the group said.

The animals were subjected to different tests based on the polymerase chain reaction (PCR), which amplifies small stretches of genetic material from the SARS coronavirus and allows them be detected. Some were also tested for the presence of antibodies to the human SARS virus.

The relatively high number of positive results is unusual, the experts said. Normally just one main and a few secondary reservoirs would be expected. "These results call into question the specificity of the tests," says François Moutou, head of the French foodsafety agency's epidemiological unit and a member of the group. "It would be unusual if species as diverse as mammals, birds and reptiles were all harbouring viruses closely



Animals on sale in Guangdong's markets are offering leads to possible sources of the SARS virus.

related to the human SARS virus." Real confirmation of the presence of a SARS-related virus, and a determination of its relationship to the human SARS virus, requires isolation and sequencing of the entire viral genome, he points out.

Some groups have already done this. For example, in work to be published shortly, scientists in Hong Kong have completed DNA sequences of coronaviruses from several different species that turn out to be closely related to the human SARS virus. The WHO has recommended that this work be extended as a priority. The results so far do not indicate whether animals infected humans or vice versa, or how the virus may have jumped between species. When more such sequences are completed, an evolutionary tree for the virus could be constructed that could indicate where it first began to evolve, thus helping to identify the reservoir. Once identified, measures could be put in place to isolate it from human contact.

But even in the absence of complete information about the reservoir, the expert delegation recommended that regulations on the farming, trading and consumption of wild animals in China should be strengthened.

Meanwhile, alarm bells have been switched off in Canada, where the virus responsible for an outbreak last month of a mild respiratory illness at a nursing home in Surrey, British Columbia, has been found not to be closely related to the SARS virus.

Although symptoms of the illness had not been typical of SARS, many patient specimens had tested positive in SARS tests based on the PCR reaction. Health workers were concerned that the SARS virus could have mutated to a less virulent form, which would have implied that it mutates more rapidly than had been thought, and so could mutate back into a virulent form.

The PCR tests rely on 'primers' that correspond to short sequences of the SARS virus. The false positives occurred because the Canadian virus is a member of the same family as the SARS virus, and so shares some of its DNA. But once researchers in British Colombia had sequenced more of the virus they found differences that showed that the two were only distant cousins.